

SEQUENCE LISTING

```

<110>  Thiry, Michel
      Dheur, Ingrid

<120>  Piscirickettsia Salmonis Antigens and Use Thereof

<130>  425.1018

<140>  10/574,639
<141>  2006-09-15

<150>  PCT/IB2004/03339
<151>  2004-10-01

<150>  2003/0743
<151>  2003-10-07

<160>  19

<170>  PatentIn version 3.3

<210>  1
<211>  1314
<212>  DNA
<213>  Piscirickettsia salmonis

<220>
<221>  CDS
<222>  (1)..(1314)

<400>  1
atg aaa gta aaa atg att gtt gca gct gta gct gtt gca ggt tta aca      48
Met Lys Val Lys Met Ile Val Ala Ala Val Ala Val Ala Gly Leu Thr
1          5          10          15

gcg act gcc gca aat gcc gct gat aat ggt aag ctt caa tta caa atc      96
Ala Thr Ala Ala Asn Ala Ala Asp Asn Gly Lys Leu Gln Leu Gln Ile
          20          25          30

aac caa ttg aag gcg caa cac act caa ctt caa cag caa gtt gct aat      144
Asn Gln Leu Lys Ala Gln His Thr Gln Leu Gln Gln Gln Val Ala Asn
          35          40          45

ctg caa ggt caa gcc caa act act ggt gcc gtt cac gtt gcc gct gtt      192
Leu Gln Gly Gln Gly Gln Thr Thr Gly Ala Val His Val Gly Ala Val
          50          55          60

ggt ggt gaa cta atc tct gaa aat aac tac gat ggt cgt gcc tta gat      240
Gly Gly Glu Leu Ile Ser Glu Asn Asn Tyr Asp Gly Arg Gly Leu Asp
65          70          75          80

ctt ctt aaa tca tta gcg aaa gca gcc agc aat gca ccg tta tta act      288
Leu Leu Lys Ser Leu Ala Lys Ala Gly Ser Asn Ala Pro Leu Leu Thr
          85          90          95

```

att ggt ggt acg tta gaa gct gat gcg caa atg aac cgt aac ggt aat Ile Gly Gly Thr Leu Glu Ala Asp Ala Gln Met Asn Arg Asn Gly Asn 100 105 110	336
gtt gga tct ggt tct act tct ggt gac cct tct ggc ctt aac tat act Val Gly Ser Gly Ser Thr Ser Gly Asp Pro Ser Gly Leu Asn Tyr Thr 115 120 125	384
gat gga act agc agt tct gca ttc tat tta gat act gca cgt att gat Asp Gly Thr Ser Ser Ser Ala Phe Tyr Leu Asp Thr Ala Arg Ile Asp 130 135 140	432
atc tta gcg cat gtg aat gac tgg gtt aac ggt gaa atc tcg tat gac Ile Leu Ala His Val Asn Asp Trp Val Asn Gly Glu Ile Ser Tyr Asp 145 150 155 160	480
tta aat ggt gat agt ggt ctt cac act ggt agc ctt tta gtg ggt aac Leu Asn Gly Asp Ser Gly Leu His Thr Gly Ser Leu Leu Val Gly Asn 165 170 175	528
ctc aat caa tta cca gtt tat ggt caa atc ggt aaa ttc tac cca gat Leu Asn Gln Leu Leu Pro Val Tyr Gly Gln Ile Gly Lys Phe Tyr Pro Asp 180 185 190	576
gca ggt ttg ttt gaa tta gct agt gat gat gtt tat tct tct agc tta Ala Gly Leu Phe Glu Leu Ala Ser Asp Asp Val Tyr Ser Ser Ser Leu 195 200 205	624
gtc aag cgt tat ttc cgt cca gat gcg caa aat ggt gca tct gta ggc Val Lys Arg Tyr Phe Arg Pro Asp Ala Gln Asn Gly Ala Ser Val Gly 210 215 220	672
ttc tat aaa gca ggc tta cat act tct tta act gca ttt aaa acg tct Phe Tyr Lys Ala Gly Leu His Thr Ser Leu Thr Ala Phe Lys Thr Ser 225 230 235 240	720
gct cca caa gct aat gct gct aac tat aac caa gca act agt gat tgg Ala Pro Gln Ala Asn Ala Ala Asn Tyr Asn Gln Ala Thr Ser Asp Trp 245 250 255	768
tct gca caa gcg gat tac act ttt aat gca ggt caa gtc aat gcc act Ser Ala Gln Ala Asp Tyr Thr Phe Asn Ala Gly Gln Val Asn Ala Thr 260 265 270	816
ata ggt gca ggt tac tta tct aat atg gtg aat acc aat gac agc ttc Ile Gly Ala Gly Tyr Leu Ser Asn Met Val Asn Thr Asn Asp Ser Phe 275 280 285	864
act gca aca ggt gca gga act ggt aca caa aaa gat cgg cta ccg atg Thr Ala Thr Gly Ala Gly Thr Gly Thr Gln Lys Asp Arg Leu Pro Met 290 295 300	912
gct aat gta agc gct aag att ggc ttt ggt cca ttt gaa gcc ctt gct Ala Asn Val Ser Ala Lys Ile Gly Phe Gly Pro Phe Glu Ala Leu Ala 305 310 315 320	960
act tat gct caa aca tta aaa ggt ttg gcg aat act aca ggt ggt aca	1008

Thr Tyr Ala Gln Thr Leu Lys Gly Leu Ala Asn Thr Thr Gly Gly Thr	
325 330 335	
acg aag ttg aaa gcc ttt gat tta gaa ggt gct tac cac ttc caa gct	1056
Thr Lys Leu Lys Ala Phe Asp Leu Glu Gly Ala Tyr His Phe Gln Ala	
340 345 350	
gtg aag ccg atg act gtg atg tta ggt tat agc cgt aca tat ggc ttt	1104
Val Lys Pro Met Thr Val Met Leu Gly Tyr Ser Arg Thr Tyr Gly Phe	
355 360 365	
gat aag gtt gga cct gtt gat cag ttt att gat ggt aat act gcg att	1152
Asp Lys Val Gly Pro Val Asp Gln Phe Ile Asp Gly Asn Thr Ala Ile	
370 375 380	
act atc aat aac aaa aaa gac caa tgg tta ttg ggt gta aac tct gaa	1200
Thr Ile Asn Asn Lys Lys Asp Gln Trp Leu Glu Gly Val Asn Ser Glu	
385 390 395 400	
gta ttt aag aac aca acg gtt ggt ctt gag tat gcg cgt gta ggt cag	1248
Val Phe Lys Asn Thr Thr Val Gly Leu Glu Tyr Ala Arg Val Gly Gln	
405 410 415	
ctt gat agc aca ggt act gac act aac cgc tac aac gta ttg act gcg	1296
Leu Asp Ser Thr Gly Thr Asp Thr Asn Arg Tyr Asn Val Leu Thr Ala	
420 425 430	
gat atg act gtt aag ttc	1314
Asp Met Thr Val Lys Phe	
435	
<210> 2	
<211> 438	
<212> PRT	
<213> <i>Piscirickettsia salmonis</i>	
<400> 2	
Met Lys Val Lys Met Ile Val Ala Ala Val Ala Gly Leu Thr	
1 5 10 15	
Ala Thr Ala Ala Asn Ala Ala Asp Asn Gly Lys Leu Gln Leu Gln Ile	
20 25 30	
Asn Gln Leu Lys Ala Gln His Thr Gln Leu Gln Gln Val Ala Asn	
35 40 45	
Leu Gln Gly Gln Gly Gln Thr Thr Gly Ala Val His Val Gly Ala Val	
50 55 60	
Gly Gly Glu Leu Ile Ser Glu Asn Asn Tyr Asp Gly Arg Gly Leu Asp	
65 70 75 80	

Leu Leu Lys Ser Leu Ala Lys Ala Gly Ser Asn Ala Pro Leu Leu Thr
 85 90 95

Ile Gly Gly Thr Leu Glu Ala Asp Ala Gln Met Asn Arg Asn Gly Asn
 100 105 110

Val Gly Ser Gly Ser Thr Ser Gly Asp Pro Ser Gly Leu Asn Tyr Thr
 115 120 125

Asp Gly Thr Ser Ser Ser Ala Phe Tyr Leu Asp Thr Ala Arg Ile Asp
 130 135 140

Ile Leu Ala His Val Asn Asp Trp Val Asn Gly Glu Ile Ser Tyr Asp
 145 150 155 160

Leu Asn Gly Asp Ser Gly Leu His Thr Gly Ser Leu Leu Val Gly Asn
 165 170 175

Leu Asn Gln Leu Pro Val Tyr Gly Gln Ile Gly Lys Phe Tyr Pro Asp
 180 185 190

Ala Gly Leu Phe Glu Leu Ala Ser Asp Asp Val Tyr Ser Ser Ser Leu
 195 200 205

Val Lys Arg Tyr Phe Arg Pro Asp Ala Gln Asn Gly Ala Ser Val Gly
 210 215 220

Phe Tyr Lys Ala Gly Leu His Thr Ser Leu Thr Ala Phe Lys Thr Ser
 225 230 235 240

Ala Pro Gln Ala Asn Ala Ala Asn Tyr Asn Gln Ala Thr Ser Asp Trp
 245 250 255

Ser Ala Gln Ala Asp Tyr Thr Phe Asn Ala Gly Gln Val Asn Ala Thr
 260 265 270

Ile Gly Ala Gly Tyr Leu Ser Asn Met Val Asn Thr Asn Asp Ser Phe
 275 280 285

Thr Ala Thr Gly Ala Gly Thr Gly Thr Gln Lys Asp Arg Leu Pro Met
 290 295 300

Ala Asn Val Ser Ala Lys Ile Gly Phe Gly Pro Phe Glu Ala Leu Ala
305 310 315 320

Thr Tyr Ala Gln Thr Leu Lys Gly Leu Ala Asn Thr Thr Gly Gly Thr
325 330 335

Thr Lys Leu Lys Ala Phe Asp Leu Glu Gly Ala Tyr His Phe Gln Ala
340 345 350

Val Lys Pro Met Thr Val Met Leu Gly Tyr Ser Arg Thr Tyr Gly Phe
355 360 365

Asp Lys Val Gly Pro Val Asp Gln Phe Ile Asp Gly Asn Thr Ala Ile
370 375 380

Thr Ile Asn Asn Lys Lys Asp Gln Trp Leu Leu Gly Val Asn Ser Glu
385 390 395 400

Val Phe Lys Asn Thr Thr Val Gly Leu Glu Tyr Ala Arg Val Gly Gln
405 410 415

Leu Asp Ser Thr Gly Thr Asp Thr Asn Arg Tyr Asn Val Leu Thr Ala
420 425 430

Asp Met Thr Val Lys Phe
435

<210> 3
<211> 1248
<212> DNA
<213> *Piscirickettsia salmonis*

<220>
<221> CDS
<222> (1)..(1248)

<400> 3
gct gat aat ggt aag ctt caa tta caa atc aac caa ttg aag gcg caa 48
Ala Asp Asn Gly Lys Leu Gln Leu Gln Ile Asn Gln Leu Lys Ala Gln
1 5 10 15
cac act caa ctt caa cag caa gtt gct aat ctg caa ggt caa ggc caa 96
His Thr Gln Leu Gln Gln Gln Val Ala Asn Leu Gln Gly Gln Gly Gln
20 25 30
act act ggt gcc gtt cac gtt ggc gct gtt ggt ggt gaa cta atc tct 144

Thr	Thr	Gly	Ala	Val	His	Val	Gly	Ala	Val	Gly	Gly	Glu	Leu	Ile	Ser		
		35					40					45					
gaa	aat	aac	tac	gat	ggt	cgt	ggc	tta	gat	ctt	ctt	aaa	tca	tta	gcg	192	
Glu	Asn	Asn	Tyr	Asp	Gly	Arg	Gly	Leu	Asp	Leu	Leu	Lys	Ser	Leu	Ala		
	50					55					60						
aaa	gca	ggc	agc	aat	gca	ccg	tta	tta	act	att	ggt	ggt	acg	tta	gaa	240	
Lys	Ala	Gly	Ser	Asn	Ala	Pro	Leu	Leu	Thr	Ile	Gly	Gly	Thr	Leu	Glu		
	65				70					75					80		
gct	gat	gcg	caa	atg	aac	cgt	aac	ggt	aat	gtt	gga	tct	ggt	tct	act	288	
Ala	Asp	Ala	Gln	Met	Asn	Arg	Asn	Gly	Asn	Val	Gly	Ser	Gly	Ser	Thr		
				85					90					95			
tct	ggt	gac	cct	tct	ggc	ctt	aac	tat	act	gat	gga	act	agc	agt	tct	336	
Ser	Gly	Asp	Pro	Ser	Gly	Leu	Asn	Tyr	Thr	Asp	Gly	Thr	Ser	Ser	Ser		
			100						105					110			
gca	ttc	tat	tta	gat	act	gca	cgt	att	gat	atc	tta	gcg	cat	gtg	aat	384	
Ala	Phe	Tyr	Leu	Asp	Thr	Ala	Arg	Ile	Asp	Ile	Leu	Ala	His	Val	Asn		
		115					120					125					
gac	tggt	gtt	aac	gggt	gaa	atc	tcg	tat	gac	tta	aat	gggt	gat	agt	gggt	432	
Asp	Trp	Val	Asn	Gly	Glu	Ile	Ser	Tyr	Asp	Leu	Asn	Gly	Asp	Ser	Gly		
	130					135					140						
ctt	cac	act	ggt	agc	ctt	tta	gtg	gggt	aac	ctc	aat	caa	tta	cca	gtt	480	
Leu	His	Thr	Gly	Ser	Gly	Leu	Leu	Val	Gly	Asn	Leu	Asn	Gln	Leu	Pro	Val	
	145				150					155					160		
tat	ggt	caa	atc	gggt	aaa	ttc	tac	cca	gat	gca	gggt	ttg	ttt	gaa	tta	528	
Tyr	Gly	Gln	Ile	Gly	Lys	Phe	Tyr	Pro	Asp	Ala	Gly	Leu	Phe	Glu	Leu		
				165					170					175			
gct	agt	gat	gat	gtt	tat	tct	tct	agc	tta	gtc	aag	cgt	tat	ttc	cgt	576	
Ala	Ser	Asp	Asp	Val	Tyr	Ser	Ser	Ser	Leu	Val	Lys	Arg	Tyr	Phe	Arg		
			180					185					190				
cca	gat	gcg	caa	aat	gggt	gca	tct	gta	ggc	ttc	tat	aaa	gca	ggc	tta	624	
Pro	Asp	Ala	Gln	Asn	Gly	Ala	Ser	Val	Gly	Phe	Tyr	Lys	Ala	Gly	Leu		
		195				200						205					
cat	act	tct	tta	act	gca	ttt	aaa	acg	tct	gct	cca	caa	gct	aat	gct	672	
His	Thr	Ser	Leu	Thr	Ala	Phe	Lys	Thr	Ser	Ala	Pro	Gln	Ala	Asn	Ala		
		210				215					220						
gct	aac	tat	aac	caa	gca	act	agt	gat	tggt	tct	gca	caa	gcg	gat	tac	720	
Ala	Asn	Tyr	Asn	Gln	Ala	Thr	Ser	Asp	Trp	Ser	Ala	Gln	Ala	Asp	Tyr		
	225				230					235				240			
act	ttt	aat	gca	gggt	caa	gtc	aat	gcc	act	ata	gggt	gca	gggt	tac	tta	768	
Thr	Phe	Asn	Ala	Gly	Gln	Val	Asn	Ala	Thr	Ile	Gly	Ala	Gly	Tyr	Leu		
				245				250						255			
tct	aat	atg	gtg	aat	acc	aat	gac	agc	ttc	act	gca	aca	gggt	gca	gga	816	
Ser	Asn	Met	Val	Asn	Thr	Asn	Asp	Ser	Phe	Thr	Ala	Thr	Gly	Ala	Gly		

260	265	270	
act ggt aca caa aaa gat cgg cta ccg atg gct aat gta agc gct aag			864
Thr Gly Thr Gln Lys Asp Arg Leu Pro Met Ala Asn Val Ser Ala Lys			
275	280	285	
att ggc ttt ggt cca ttt gaa gcc ctt gct act tat gct caa aca tta			912
Ile Gly Phe Gly Pro Phe Glu Ala Leu Ala Thr Tyr Ala Gln Thr Leu			
290	295	300	
aaa ggt ttg gcg aat act aca ggt ggt aca acg aag ttg aaa gcc ttt			960
Lys Gly Leu Ala Asn Thr Thr Gly Gly Thr Lys Leu Lys Ala Phe			
305	310	315	320
gat tta gaa ggt gct tac cac ttc caa gct gtg aag ccg atg act gtg			1008
Asp Leu Glu Gly Ala Tyr His Phe Gln Ala Val Lys Pro Met Thr Val			
325	330	335	
atg tta ggt tat agc cgt aca tat ggc ttt gat aag gtt gga cct gtt			1056
Met Leu Gly Tyr Ser Arg Thr Tyr Gly Phe Asp Lys Val Gly Pro Val			
340	345	350	
gat cag ttt att gat ggt aat act gcg att act atc aat aac aaa aaa			1104
Asp Gln Phe Ile Asp Gly Asn Thr Ala Ile Thr Ile Asn Asn Lys Lys			
355	360	365	
gac caa tgg tta ttg ggt gta aac tct gaa gta ttt aag aac aca acg			1152
Asp Gln Trp Leu Leu Gly Val Asn Ser Glu Val Phe Lys Asn Thr Thr			
370	375	380	
gtt ggt ctt gag tat gcg cgt gta ggt cag ctt gat agc aca ggt act			1200
Val Gly Leu Glu Tyr Ala Arg Val Gly Gln Leu Asp Ser Thr Gly Thr			
385	390	395	400
gac act aac cgc tac aac gta ttg act gcg gat atg act gtt aag ttc			1248
Asp Thr Asn Arg Tyr Asn Val Leu Thr Ala Asp Met Thr Val Lys Phe			
405	410	415	
 <210> 4			
<211> 416			
<212> PRT			
<213> <i>Piscirickettsia salmonis</i>			
 <400> 4			
Ala Asp Asn Gly Lys Leu Gln Leu Gln Ile Asn Gln Leu Lys Ala Gln			
1	5	10	15
His Thr Gln Leu Gln Gln Gln Val Ala Asn Leu Gln Gly Gln Gly Gln			
20	25	30	
Thr Thr Gly Ala Val His Val Gly Ala Val Gly Gly Glu Leu Ile Ser			
35	40	45	

Glu Asn Asn Tyr Asp Gly Arg Gly Leu Asp Leu Leu Lys Ser Leu Ala
50 55 60

Lys Ala Gly Ser Asn Ala Pro Leu Leu Thr Ile Gly Gly Thr Leu Glu
65 70 75 80

Ala Asp Ala Gln Met Asn Arg Asn Gly Asn Val Gly Ser Gly Ser Thr
85 90 95

Ser Gly Asp Pro Ser Gly Leu Asn Tyr Thr Asp Gly Thr Ser Ser Ser
100 105 110

Ala Phe Tyr Leu Asp Thr Ala Arg Ile Asp Ile Leu Ala His Val Asn
115 120 125

Asp Trp Val Asn Gly Glu Ile Ser Tyr Asp Leu Asn Gly Asp Ser Gly
130 135 140

Leu His Thr Gly Ser Leu Leu Val Gly Asn Leu Asn Gln Leu Pro Val
145 150 155 160

Tyr Gly Gln Ile Gly Lys Phe Tyr Pro Asp Ala Gly Leu Phe Glu Leu
165 170 175

Ala Ser Asp Asp Val Tyr Ser Ser Ser Leu Val Lys Arg Tyr Phe Arg
180 185 190

Pro Asp Ala Gln Asn Gly Ala Ser Val Gly Phe Tyr Lys Ala Gly Leu
195 200 205

His Thr Ser Leu Thr Ala Phe Lys Thr Ser Ala Pro Gln Ala Asn Ala
210 215 220

Ala Asn Tyr Asn Gln Ala Thr Ser Asp Trp Ser Ala Gln Ala Asp Tyr
225 230 235 240

Thr Phe Asn Ala Gly Gln Val Asn Ala Thr Ile Gly Ala Gly Tyr Leu
245 250 255

Ser Asn Met Val Asn Thr Asn Asp Ser Phe Thr Ala Thr Gly Ala Gly
260 265 270

Thr Gly Thr Gln Lys Asp Arg Leu Pro Met Ala Asn Val Ser Ala Lys
 275 280 285

Ile Gly Phe Gly Pro Phe Glu Ala Leu Ala Thr Tyr Ala Gln Thr Leu
 290 295 300

Lys Gly Leu Ala Asn Thr Thr Gly Gly Thr Thr Lys Leu Lys Ala Phe
 305 310 315 320

Asp Leu Glu Gly Ala Tyr His Phe Gln Ala Val Lys Pro Met Thr Val
 325 330 335

Met Leu Gly Tyr Ser Arg Thr Tyr Gly Phe Asp Lys Val Gly Pro Val
 340 345 350

Asp Gln Phe Ile Asp Gly Asn Thr Ala Ile Thr Ile Asn Asn Lys Lys
 355 360 365

Asp Gln Trp Leu Leu Gly Val Asn Ser Glu Val Phe Lys Asn Thr Thr
 370 375 380

Val Gly Leu Glu Tyr Ala Arg Val Gly Gln Leu Asp Ser Thr Gly Thr
 385 390 395 400

Asp Thr Asn Arg Tyr Asn Val Leu Thr Ala Asp Met Thr Val Lys Phe
 405 410 415

<210> 5

<400> 5
 000

<210> 6

<400> 6
 000

<210> 7

<400> 7
 000

<210> 8

<400> 8
 000

<210> 9

```

<400> 9
000

<210> 10

<400> 10
000

<210> 11

<400> 11
000

<210> 12

<400> 12
000

<210> 13

<400> 13
000

<210> 14

<400> 14
000

<210> 15

<400> 15
000

<210> 16

<400> 16
000

<210> 17

<400> 17
000

<210> 18

<400> 18
000

<210> 19
<211> 2092
<212> DNA
<213> Piscirickettsia salmonis

<400> 19

```

ccaagaacta tcaaaaacta tataggcaaa gtataaagtc tgaagcttaa cctttgctta	60
aatgtacatc aggcttaagg tgatttctgt tgagtatttt cagagtctta agtcaatttt	120
aatctttctt aagggtgaaa acaggctaaa atcaacattt tgataaaatt attaatTTTT	180
ttttattgtt cttttttaat cggtttttat cctaatttga tagatagtta tcgaaattca	240
ataagttttg tttttaattg aatttttttt acgagtttgg gttttacaaa gtgaatttac	300
ctgggtatag tagccccagt tgcttaatag cacttaaagt tgtatccaga taaaacaag	360
ttagggtaaa aagaatgaaa gtaaaaatga ttgttgagc tgtagctgtt gcagggttaa	420
cagcgactgc cgcacaatgcc gctgataatg gtaagcttca attacaaatc aaccaattga	480
aggcgcaaca cactcaactt caacagcaag ttgctaattc gcaagggtcaa ggcacaacta	540
ctgggtgccg tcacgttggc gctgttgggt gtgaactaat ctctgaaaat aactacgatg	600
gtcgtggcct agatcttctt aaatcattag cgaaagcagg cagcaatgca ccgtatttaa	660
ctattgggtg tacgttagaa gctgatgcgc aaatgaaccg taacggtaat gttggatctg	720
gttctacttc tggtagccct tctggcctta actatactga tgggaactagc agttctgcat	780
tctatttaga tactgcacgt attgatattc tagcgcatgt gaatgactgg gttaacgggtg	840
aaatctcgta tgacttaaat ggtgatagtg gtcttcacac tggtagcctt tttagtgggta	900
acctcaatca attaccagtt tatggtcaaa tcggtaaatt ctaccagat gcaggtttgt	960
ttgaattagc tagtgatgat gtttattctt cttagcttagt caagcggtat ttccgtccag	1020
atcgcaaaaa tgggtcatct gtaggcttct ataaagcagg ctacatact tctttaactg	1080
catttaaaaa gtctgctcca caagctaatt ctgctaacta taaccaagca actagtgatt	1140
ggtctgcaca agcggattac acttttaatt cagggtcaagt caatgccact atagggtgag	1200
gttacttatc taatatgggt aataccaatg acagcttcac tgcaacagggt gcagggaactg	1260
gtacacaaaa agatcggtca ccgatggcta atgtaagcgc taagattggc ttgggtccat	1320
ttgaagccct tgctacttat gctcaaacta taaaaggttt ggcgaatact acagggtggt	1380
caacgaagtt gaaagccttt gatttagaag gtgcttacca ctccaagct gtgaagccga	1440
tgactgtgat gttaggttat agcgtacatc atggctttga taaggttgga cctgttgatc	1500
agtttattga tggtaatact gcgattacta tcaataacaa aaaagaccaa tggttattgg	1560
gtgtaaaact tgaagtattt aagaacacaa cggttgggtc tgagtatgag cgtgtaggtc	1620
agcttgatag cacaggtagt gacactaacc gctacaacgt attgactgag gatagtactg	1680
ttaaagtctc atttaagaac tttaaagttt tcaaaaaggc gctgcggcgc ctttttttat	1740

gggcgttaat tattggtaat gtaggctagt atttaaattt gtgagtgatg agagatgaaa	1800
aatttaaatct atgcacagcg ttgctttat ttgccgtat tgattgcggt gattgtcacc	1860
tttgttcagc catttctaata gcgattaag cttgctgatg tgcctttaat gccgctcgtg	1920
gtcgttcga tttattcctt gatttttgct gcagctttag cattagctgc atataaatta	1980
cgcagcaaaag ctggttgccc gcggtttttg ttggtgattt tattttattgg gcatgcgatg	2040
cctgcggtaa aaaactggct agtgccttgg catacgcgg agctttttgc ga	2092